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#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/021,121

DATE: 02/01/2002
TIME: 11:33:53

Input Set : N:\Crf3\RULE60\10021121.raw
Output Set: N:\CRF3\02012002\J021121.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Caras, Ingrid W

7 (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

9 (iii) NUMBER OF SEQUENCES: 10

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Genentech, Inc.

13 (B) STREET: 1 DNA Way

14 (C) CITY: South San Francisco

15 (D) STATE: California

16 (E) COUNTRY: USA

17 (F) ZIP: 94080

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

C--> 26 (A) APPLICATION NUMBER: US/10/021,121

C--> 27 (B) FILING DATE: 06-Dec-2001

28 (C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/635,130

32 (B) FILING DATE: 19-Mar-1996

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Torchia, PhD., Timothy E.

37 (B) REGISTRATION NUMBER: 36,700

38 (C) REFERENCE/DOCKET NUMBER: P1001

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 650/225-8674

42 (B) TELEFAX: 650/952-9881

43 (2) INFORMATION FOR SEQ ID NO: 1:

45 (i) SEQUENCE CHARACTERISTICS:

46 (A) LENGTH: 1877 base pairs

47 (B) TYPE: Nucleic Acid

48 (C) STRANDEDNESS: Double

49 (D) TOPOLOGY: Linear

51 (ix) FEATURE:

52 (A) NAME/KEY: Extra Cellular Domain

53 (B) LOCATION: 244-899

54 (C) IDENTIFICATION METHOD:

55 (D) OTHER INFORMATION:

57 (ix) FEATURE:

ENTERED

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58 (A) NAME/KEY: Transmembrane Domain
59 (B) LOCATION: 901-978
60 (C) IDENTIFICATION METHOD:
61 (D) OTHER INFORMATION:
63 (ix) FEATURE:
64 (A) NAME/KEY: signal peptide
65 (B) LOCATION: 244-321
66 (C) IDENTIFICATION METHOD:
67 (D) OTHER INFORMATION:
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 GNTCTAGAAN TAGTGGATCC CCCCCGGGCTG CAGGAATTCC GACGGGCCCT 50
74 GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
76 CAGGAAGCAG GTCCCGCTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
78 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
80 TTTGGGGAG TTGGTCCCCC GCCCCCCCAGG CCTTGGCGGG GTC ATG 246
81 Met
82 1
84 GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
85 Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
86 5 10
88 GCC CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
89 Ala Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
90 15 20 25
92 CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
93 Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
94 30 35 40
96 AGG TTC CAG GCA GAG GGT TAT GTG CTG TAC CCT CAG 402
97 Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
98 45 50
100 ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
101 Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
102 55 60 65
104 CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480
105 Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
106 70 75
108 AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519
109 Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
110 80 85 90
112 GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
113 Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
114 95 100 105
116 CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
117 Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
118 110 115
120 GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
121 Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
122 120 125 130
124 CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
125 His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr

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126	135	140
128	CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA	714
129	Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu	
130	145	150
132	155	
133	ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT	753
134	Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser	
136	160	165
137	170	
138	CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA	792
139	Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu	
140	175	180
141	ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG	831
142	Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu	
143	185	190
144	195	
145	GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC	870
146	Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser	
147	200	205
148	205	
149	AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT	909
150	Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro	
151	210	215
152	220	
153	CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG	948
154	Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu	
155	225	230
156	235	
157	GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC	987
158	Ala Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala	
159	240	245
160	ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT	1026
161	Met Cys Trp Arg Arg Arg Ala Lys Pro Ser Glu Ser	
162	250	255
163	260	
164	CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT	1065
165	Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser	
166	265	270
167	270	
168	CTG GGC CTG GGG GGT GGA GGT ATG GGA CCT CGG GAG	1104
169	Leu Gly Leu Gly Gly Gly Met Gly Pro Arg Glu	
170	275	280
171	285	
172	GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC	1143
173	Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly	
174	290	295
175	300	
176	GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG	1182
177	Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys	
178	305	310
179	310	
180	GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG	1221
181	Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln	
182	315	320
183	325	
184	GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA	1260
185	Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr	
186	330	335
187	335	
188	TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA	1299
189	Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile	
190	340	345
		350

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192 CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338
193 Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr
194 355 360 365
196 ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
197 Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
198 370 375
200 TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416
201 Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro
202 380 385 390
204 TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455
205 Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg
206 395 400
208 ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG 1494
209 Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr
210 405 410 415
212 GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT CTT GGG AGG 1533
213 Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
214 420 425 430
216 CTG AAT ATG CAT CAG ACA CTG CTC CGG CAA CGG GCC 1572
217 Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala
218 435 440
220 AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
221 Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
222 445 450 455
224 ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660
226 GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710
228 CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTAA 1760
230 TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTG TGCTGCCTGT 1810
232 CAGCTCTGTG CTACCTGGCA GTTCCCCCTCA TGGAATTGCA TATCAAGCTT 1860
234 ATCGATACCG TCGACCT 1877
236 (2) INFORMATION FOR SEQ ID NO: 2:
238 (i) SEQUENCE CHARACTERISTICS:
239 (A) LENGTH: 455 amino acids
240 (B) TYPE: Amino Acid
241 (D) TOPOLOGY: Linear
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
245 Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
246 1 5 10 15
248 Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
249 20 25 30
251 Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
252 35 40 45
254 Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
255 50 55 60
257 Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
258 65 70 75
260 Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
261 80 85 90
263 Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Thr Cys Asp

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264	95	100	105
266	Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln Glu Tyr		
267	110	115	120
269	Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser His His Asp Tyr		
270	125	130	135
272	Tyr Ile Ile Ala Thr Ser Asp Gly Thr Arg Glu Gly Leu Glu Ser		
273	140	145	150
275	Leu Gln Gly Gly Val Cys Leu Thr Arg Gly Met Lys Val Leu Leu		
276	155	160	165
278	Arg Val Gly Gln Ser Pro Arg Gly Gly Ala Val Pro Arg Lys Pro		
279	170	175	180
281	Val Ser Glu Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser		
282	185	190	195
284	Leu Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser Asn		
285	200	205	210
287	Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro Pro Ser Met		
288	215	220	225
290	Pro Ala Val Ala Gly Ala Ala Gly Gly Leu Ala Leu Leu Leu Leu		
291	230	235	240
293	Gly Val Ala Gly Ala Gly Gly Ala Met Cys Trp Arg Arg Arg Arg		
294	245	250	255
296	Ala Lys Pro Ser Glu Ser Arg His Pro Gly Pro Gly Ser Phe Gly		
297	260	265	270
299	Arg Gly Gly Ser Leu Gly Leu Gly Gly Gly Gly Met Gly Pro		
300	275	280	285
302	Arg Glu Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly		
303	290	295	300
305	Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys Val Ser		
306	305	310	315
308	Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro Pro		
309	320	325	330
311	Gln Ser Pro Pro Asn Ile Tyr Tyr Thr Ser Ile Ser Val Leu Glu		
312	335	340	345
314	Trp Pro Ile Leu His Thr Ile Gln Leu Phe Phe Met Arg Ser Lys		
315	350	355	360
317	Cys Ser Arg Val Thr Thr Phe Leu Phe Pro Val Gln Val Ile Thr		
318	365	370	375
320	Thr Ser Thr Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn		
321	380	385	390
323	Pro Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg Ile		
324	395	400	405
326	Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr Ala Leu Phe		
327	410	415	420
329	Val Leu Val Leu Ile Leu Leu Gly Arg Leu Asn Met His Gln		
330	425	430	435
332	Thr Thr Leu Leu Arg Gln Arg Ala Ser Val Glu Ala Glu Ala Gly		
333	440	445	450
335	Gln His Gly Pro Leu		
336	455		

VERIFICATION SUMMARY

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L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]